Appl. No.:   09/943,579
Amdt. dated April 1, 2004
Reply to Office Action of January 16, 2004

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1.   (Currently amended) A computerComputer apparatus for gene prediction comprising:

a processor that is adapted to execute instructions that cause the processor to

create a plurality of units for that predict predicting gene locations in a subject genomic sequence, wherein each unit of said units is capable of providing respective intermediate indications of gene locations output by the unit; and

create a combiner coupled to each unit to receive the that receives said respective intermediate output indications of predicted gene locations, the combiner being formed of a comprising a Bayesian network which combines the predicted that combines said intermediate indications of gene locations using probabilities of gene locations of the subject genomic sequence[[,]] and forming to form a final combined output for indicating predicted genes gene locations in of the subject genomic sequence.

2.   (Currently amended) The Computer computer apparatus as claimed in claim 1 wherein the plurality of units is a plurality of expert systems.

3.   (Currently amended) The Computer computer apparatus as claimed in claim 1 wherein the Bayesian network accounts for includes probabilistic dependencies between individual units and dependencies between adjacent parts of the subject genomic sequence.

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4.   (Currently amended) The ~~Computer~~ computer apparatus as claimed in claim 3 wherein the Bayesian network combines the predicted gene locations according to

$$Y^* = \max_{Y_t} P(Y_t | E_1, \ldots, E_n, Y^*_{t-1})$$
$$E_i \, \varepsilon \, \{E, I\}$$

where t is location in the subject genomic sequence and $E_1, \ldots, E_n$ are the respective predictions (E for exon or I for intron ~~or intergenic region~~) made by individual units 1 through n, n being the number of units in the plurality.

5.   (Currently amended) The ~~Computer~~ computer apparatus as claimed in claim 1 wherein the subject genomic sequence is a DNA or RNA sequence.

6.   (Currently amended) The ~~Computer~~ computer apparatus as claimed in claim 1 wherein gene locations include exon predictions.

7.   (Withdrawn) Computer apparatus as claimed in claim 6 wherein gene locations further include exon and intron predictions; and the final combined output indicates exons and introns of the predicted genes of the subject genomic sequence.

8.   (Currently amended) The ~~Computer~~ computer apparatus as claimed in claim 1 wherein the Bayesian network comprises a table or set of probabilities of a given sub-sequence being a protein encoding exon prepared by applying training data to the computer apparatus, wherein said training data comprises character strings representing ~~is trained on~~ known genes of a known genome sequence.

9.   (Currently amended) A method for automated gene prediction, comprising the steps of:

obtaining from a plurality of expert systems a plurality of respective preliminary gene location predictions for a subject gene in a subject genomic

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~~sequence using a plurality of expert systems, preliminarily predicting gene locations in a subject genomic sequence;~~

inputting into a digital processor programmed to contain a Bayesian network a plurality of respective datasets representing said gene location predictions;

combining said respective datasets in said Bayesian network ~~using a Bayesian network, combining the preliminarily predicted gene locations~~; and

~~to form~~ forming from said Bayesian network a ~~final combined~~ data output indicating an improved predicted ~~genes~~ location for said subject gene in ~~of~~ the subject genomic sequence, wherein the Bayesian network includes probabilistic dependencies between individual expert systems and dependencies between adjacent parts of the subject genomic sequence ~~accounting for dependencies between individual expert systems and dependencies between adjacent parts of the subject genomic sequence.~~

10.   (Currently amended) [[A]]The method as claimed in claim 9 wherein ~~the step of combining using a~~ said Bayesian network combines said plurality of datasets according to the probability equation

$$Y^*=\max_{Yt}P(Y_t|E_1, \ldots , E_n, Y^*_{t-1})$$

$$E_i \, \varepsilon \, \{E,I\}$$

~~where~~ wherein t is location of a subject gene in the subject genomic sequence and $E_1, \ldots, E_n$ are the respective predictions (E for exon or I for intron ~~or intergenic region~~) made by individual expert systems, n being the number of expert systems in the plurality.

11.   (Currently amended) [[A]]The method as claimed in claim 9 wherein the subject genomic sequence is a DNA or RNA sequence.

12.   (Currently amended) [[A]]The method as claimed in claim 9 wherein said obtaining and said inputting each comprise predicting an exon location ~~gene locations include exon predictions.~~

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13.   (Withdrawn) A method as claimed in claim 12 wherein gene locations further include exon and intron predictions; and the final combined output indicates exons and introns of the predicted genes of the subject genomic sequence.

14.   (New) The method of claim 9 wherein said forming comprises creating from said Bayesian network a data output indicating an optimal combined predicted location for each said subject gene in the subject genomic sequence.

15.   (New) The method of claim 9 comprising, prior to said combining,

providing a training dataset to said processor representing a plurality of known gene locations on a known genomic sequence.

16.   (New) The method of claim 15 comprising,

constructing a conditional probability function or table from said training dataset.

17.   (New) The method of claim 9 comprising selecting a subject gene that is unknown to said expert systems.

18.   (New) A computer apparatus comprising means for performing the method of claim 9.